



1 CGAGGCCACGGCTTATGCAAGCAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT  
-----+-----+-----+-----+-----+-----+-----+  
71 AGATGAACTCATGACTGTACTCTACCCAGAATATTGGAATAATGTACAAGTGTCAAGCTAAG  
-----+-----+-----+-----+-----+-----+-----+  
M T V L Y P E Y W K M Y K C Q L R  
121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC  
-----+-----+-----+-----+-----+-----+-----+  
K G G W Q H N R E Q A N L N S R T E E T  
181 TATAAAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG  
-----+-----+-----+-----+-----+-----+-----+  
I K F A A A H Y N T E I L K S I D N E W  
241 GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGGAGT  
-----+-----+-----+-----+-----+-----+-----+  
R K T Q C M P R E V C I D V G K E F G V  
301 CGGACAAACACCTTCTTTAAACCTCCATGTGTCTCCGTCACAGATGTGGGGTGTGCTG  
-----+-----+-----+-----+-----+-----+-----+  
A T N T F F K P P C V S V Y R C G G C C

FIG. 2A

361 CAATAGTGGGGCTGCAGTGCATGAACACACGACGAGCTACCTCAGCAAGACGTTATT  
-----+-----+-----+-----+-----+-----+-----+  
N S E G L Q C M N T S T S Y L S K T L F  
421 TGAAATTACAGTGCCCTCTCTCTCAAGGCCCCAAACACAGTAACAATCAGTTTGGCCAATCA  
-----+-----+-----+-----+-----+-----+-----+  
E I T V P L S Q G P K P V T I S F A N H  
481 CACTTCCTGCCGATGCTCTAACTGGATGTTACAGACAAGTTCATTCCATTATTAG  
-----+-----+-----+-----+-----+-----+-----+  
T S C R C M S K L D V Y R Q V H S I I R  
541 ACGTTCCCTGCCAGCAACACTACCACAGTGTCTCAGGCAGCGAACAAGACCTGCCCCACCCAA  
-----+-----+-----+-----+-----+-----+-----+  
R S L P A T L P Q C Q A A N K T C P T N  
601 TTACATGTGGAATAATCACATCTGCAGATGCCCTGGCTCAGGAAGATTTATGTTTCCTC  
-----+-----+-----+-----+-----+-----+-----+  
Y M W N N H I C R C L A Q E D F M F S S  
661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAACAAGGAGCT  
-----+-----+-----+-----+-----+-----+-----+  
D A G D D S T D G F H D I C G P N K E L

FIG. 2B

721 GGATGAAGAGACCTGTCAAGTGTCTGCAGAGCGGGGCTTCGGCCCTGCCAGCTGTGGACC  
-----+-----+-----+-----+-----+-----+  
D E E T C Q C V C R A G L R P A S C G P  
781 CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAACAACTCTTCCCCCAG  
-----+-----+-----+-----+-----+-----+  
H K E L D R N S C Q C V C K N K L F P S  
841 CCAATGTGGGGCCCAACCGAGAAATTGTATGAAACACATGCCAGTGTATGTAAAGAAC  
-----+-----+-----+-----+-----+-----+  
Q C G A N R E F D E N T C Q C V C K R T  
901 CTGCCCCAGAAATCAACCCCTAAATCCTCGAAATGTGCCTGTGAATGTACAGAAAGTCC  
-----+-----+-----+-----+-----+-----+  
C P R N Q P L N P G K C A C E C T E S P  
961 ACAGAAATGCTTGTAAAGGAAAGAGTTCCACCACCAACATGCAGCTGTTACAGACG  
-----+-----+-----+-----+-----+-----+  
Q K C L L K G K K F H H Q T C S C Y R R  
1021 GCCATGTACGAACCGCCAGAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG  
-----+-----+-----+-----+-----+-----+  
P C T N R Q K A C E P G F S Y S E E V C

FIG. 2C

```

1081 TCGTTGTGCCCTTCATATTGGCAAAGACCACAAATGAGCTAAGATTGTAAGTTTCCCA
      R C V P S Y W Q R P Q M S
1141 GTTCATCGATTTTCTATTATGGAATACTGTGTGCCACAGTAGAAGTGTCTGTGAACAGA
1201 GAGACCCCTTGTGGTCCCATGCTAACAAAGACAAAAGTCTGTCTTTTCCCTGAACCATGTGGA
1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGCAAAAGGCCCTCTTGTAAGACTGGTTT
1321 CTGCCAATGACCAACACAGCCCAAGATTTTCCCTCTTGATTTTCTTAAAGAAATGACTATA
1381 TAATTTATTCCACTAAAAATATTGTTTCTGCAATTCATTTTATAGCAACAACAATTGGT
1441 AAACTCAGTGATCAATATTTTATATCATGCATAAATATGTTTAAATAAAATGAAAA
1501 TTGTATTATAAAAAAATAAAAAA

```

FIG. 2D



1 CGAGGCCACGGCTTATGCAAGCAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT  
-----+-----+-----+-----+-----+-----+-----+  
71 AGATGAACCTCATGACTGTACTCTACCCAGAAATATTGGAAAATGTACAAGTGTACAGCTAAG  
-----+-----+-----+-----+-----+-----+-----+  
M T V L Y P E Y W K M Y K C Q L R  
-----+-----+-----+-----+-----+-----+-----+  
121 GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAAGAGAC  
-----+-----+-----+-----+-----+-----+-----+  
K G G W Q H N R E Q A N L N S R T E E T  
-----+-----+-----+-----+-----+-----+-----+  
181 TATAAAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG  
-----+-----+-----+-----+-----+-----+-----+  
I K F A A A H Y N T E I L K S I D N E W  
-----+-----+-----+-----+-----+-----+-----+  
241 GAGAAAGACTCAATGCATGCCACGGAGGTGTATAGATGTGGGAAGGAGTTTGAGT  
-----+-----+-----+-----+-----+-----+-----+  
R K T Q C M P R E V C I D V G K E F G V  
-----+-----+-----+-----+-----+-----+-----+  
301 CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCTCGTCTACAGATGTGGGGGTTGCTG  
-----+-----+-----+-----+-----+-----+-----+  
A T N T F F K P P C V S V Y R C G G C C  
-----+-----+-----+-----+-----+-----+-----+

FIG. 2A